



Ortholog prediction of the *Aspergillus* genus applicable for synthetic biology

Rasmussen, Jane Lind Nybo; Vesth, Tammi Camilla; Theobald, Sebastian; Frisvad, Jens Christian; Grigoriev, Igor V.; Baker, Scott E.; Andersen, Mikael Rørdam

Publication date:
2016

Document Version
Early version, also known as pre-print

[Link back to DTU Orbit](#)

Citation (APA):
Rasmussen, J. L. N., Vesth, T. C., Theobald, S., Frisvad, J. C., Grigoriev, I. V., Baker, S. E., & Andersen, M. R. (2016). *Ortholog prediction of the Aspergillus genus applicable for synthetic biology*. Abstract from Cell Symposia: Technology. Biology. Data Science 2016, Berkeley, United States.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Ortholog prediction of the *Aspergillus* genus applicable for synthetic biology

Jane Nybo (1), Tammi C. Vesth (1), Sebastian Theobald (1), Jens C. Frisvad (1), Igor V. Grigoriev (3), Scott E. Baker (2), Mikael R. Andersen (1)

1) Department of Systems Biology, Technical University of Denmark, Kgs. Lyngby, Denmark

2) Joint Bioenergy Institute, Berkeley, CA, USA

3) Joint Genome Institute, Walnut Creek, CA, USA

The *Aspergillus* genus contains leading industrial microorganisms, excelling in producing bioactive compounds and enzymes. Using synthetic biology and bioinformatics, we aim to re-engineer these organisms for applications within human health, pharmaceuticals, environmental engineering, and food production. In this project, we compare the genomes of +300 species from the *Aspergillus* genus to generate a high-resolution pan-genomic map, representing genetic diversity spanning ~200 million years. We are identifying genes specific to species and clades to allow for guilt-by-association-based mapping of genotype-to-phenotype. To achieve this, we have developed orthologous protein prediction software that utilizes genus-wide genetic diversity. The approach is optimized for large datasets, based on BLASTp considering protein identity and alignment coverage, and clustering using single linkage of bi-directional hits. The result is orthologous protein families describing the genomic and functional features of individual species, clades and the core/pan genome of *Aspergillus*; and applicable to genotype-to-phenotype analyses in other microbial genera.